Figure 1A

AACTATIGAAGTGAACTGGAATAAAGCAGACTCCAGGAGAGGGTTTACAGTGGATGGA	
TACCTCACTTGACCTATTTCGTCTGAGAGAGGGTTTTACAGTGGATGGGCTGGATAAACCCCAACACTGGAGAGCCAACATTTTACTCCTAAGGAGCCAACACTGGAGAGCCAACACTGGAGAGCCAACATTTTACTCCTAAGGAGCCTAATTTTGGAGAGAGCCTAATTTTGGAAAACCTTAAAAAAAA	YFCSRSKGKNEAMFAYNGQGTLVTV
TACCTCACTTGACCTATTTCGTCTGAGGGCTCCCCAAATGTCACCTACCCGACCTATTTGGGTTGTACCTCTCGGTTGTAATGTCACCTACCCGACCTATTTGGGTTCTTGAGGTCCTCCCCAAATGTCACCTACCCGACCTATTTGGGTTTGTACCTCTCGGTTGTAATGTCACCTACCT	100A B K
ATGGAGTGAACTGGATAAAGCAGACTCCAGGAGAGGGTTTACAGTGGATGGA	TACCCATGTATAAAGACAAGTTCTAGCTCCCCATTTTTGCTTCGGACCAAACGAATAACCCCGGTTCCCTGAGACCAGTGACAGAGACTT
ATGGAGTGAACTGGAGAACACTCCAGGAGAGGGTTTACAGTGGATGAGCCTACTGGAGAACACTGGAGAGCCAACACTTACCTCACTTGACCTGAACACTGGAGAGCCAACACTTACCTCACTTGACCTTATTTCGTCTGAGGTCCTCTCCCAAATGTCACCTTACCCGACCTATTTTGGGTTTGTGACCTCTCGGTTGTAAACCTCTCGGTTGTAAACCTCAAAAATGTCAAAAATGTCACCTACCGACCTATTTTGGGGTTGTGACCTCTCGGTTGTAAAAATGTAAAAATGTAAAAATGAAGATTCCCTCAAAAAAATGAAGAACCTTCAAAAAATGAAGAACCTTCAAAAAATGAAGAACCTTAAGGAAAACCTTAAAAAATGAAGAACCTTAAGAAACCTTAAGAAACCTTAAGAAACCTTAAGAAACCTTAAGAAACTTACTCCTTAAGAAACCTTAAGAAACCTTAAGAAAAATGAAGAAAAAATGAAGAAAAAAAA	
ATGGAGTGAACTGGAGAACACTCCAGGAGAGGGTTTACAGTGGATGAGCCTGGATAAACCCCAACACTGGAGAGCCAACACTT  TACCTCACTTGACCTATTTCGTCTGAGGTCCTCTCCCAAATGTCACCTACCCGACCTATTTGGGGTTGTGACCTCTCGGTTGTAA  40  Y G V N W I K Q T P G E G L Q W M G W I N P N T G B P T F  CDR1  ATGGACTTCAAGGGAACGATTTGCCTTCTCTCTTTGGAATCCTCTGCCAGCACTGTTTTTGCAGATCCAGCAACACTTAAAAATGAGGA  TACTGAAGTTCCCTGCTAAACGGAAGGAAACCTTAAGGAGAGACGGTCGTGACGGAAAAAACGTCTAGTCGTTGGAAGTTTTTACTCCT  10  11  12  13  14  15  16  17  18  17  18  18  18  18  18  18  18	
ATGGAGTGAACTGGATAAAGCAGACTCCAGGAGAGGGTTTACAGTGGATGGGCTGGATAAACCCCAACACTGGAGAGCCAACATT TACCTCACTTGACCTATTTCGTCTGAGGTCCTCTCCCAAATGTCACCTACCCGACCTATTTGGGGTTGTGACCTCTCGGTTGTAA  40  Y G V N W I K Q T P G E G L Q W M G W I N P N T G B P T F CDR1  ATGACTTCAAGGGACGATTTGCCTTCTCTTTGGAATCCTCTGCCAGCACTGCCTTTTTGCAGATCAGCAACCTCAAAAATGAGGA	ACTACTGAAGTTCC
ATGGAGTGAACTGGATAAAGCAGACTCCAGGAGAGGGTTTACAGTGGATGGA	GATGATGACTTCAAGGGACGATTTGCCTTCTCTTTGGAATCCTCTGCCAGCACTGCCTTTTTTGCAGATCAGCAACCTCAAAAATGAGGAC
ATGGAGTGAACTGGATAAAGCAGACTCCAGGAGAGGGTTTACAGTGGATGGA	CDR1 CDR2
ATGGAGTGAACTGGATAAAGCAGACTCCAGGAGAGGGTTTACAGTGGATGAGCTGGATAAACCCCAACACTGGAGAGCCAACATT +++++	TO THE TOTAL SO S2A
atogagigaaciggataaagcagaciccaggagaggggittacagiggaigggciggajaaaccccaacaciggagagccaacatt	TTGATACCTCACTIGACCTATTTCGTCTGAGGTCCTCTCCCAAATGTCACCTACCCGACCTATTTGGGGTTGTGACCTCTCGGTTGTAAA
	CCAACACT
I Q L V Q S G P E L K K P G E T V K V T C K T S G Y T F T	LVQSGPELKKPGETVKVTCKTSGYT
AGGTCAACCACGTCAGACCTGGACTTCTTCGGACCTCTCTGTCAGTTCCAGTGGACGTTCTGAAGACCTATATGGAAGTG 30	CGACTTCTTCGGACCTCTCTGTCAGTTC
CAGATCCAGTTGGTGCAGTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGGTCACCTGCAAGACTTCTGGATATACCTTCACA	ασγασασαφήσετο + ο γραφη το επιτεριστεριστεριστο + ο γραφη στο + ο γραφη στο + ο γραφη στο + ο γραφη στο + ο γ

Figure 1B

Figure 2A

MGTYFCSR <mark>SRGKNBAWFAY</mark> WGQGTLVTVSS 113	B&EEII ATGGGTACATATTTCTGTTCAAGATCGAGGGGTAAAAACGAAGCCTGGTTTGCTTATTGGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA TACCCCATG TATAAAGACAAGTTCTAGCTCCCCATTTTTGCTTCGGACCAAACGAATAACCCCGGTTCCCTGAGA <u>CCAGTGG</u> CAGAGGAGT	DDDFKGRFAFSLESSASTAFLQISNLKNED 8	GATGATGACTTCAAGGGACGATTTGCCTTCTCTTTGGAATCCTCTGCCAGCACTGCCTTTTTTGCAGATCAGCAACCTCAAAAATGAGGAC CTACTACTGAAGTTCCCTGCTAAACGGAAGAGAAACCTTAGGAGAGACGTCGTGACGGAAAAACGTCTAGTCGTTGGAGTTTTTACTCCTG	NYGVNWIKOTPGEGLOWMGWINPNTGEPTP 55 CDR1 CDR2	AACTATIGGAGTGAACTGGATAAAGCAGACTCCAGGAGAGGGTTTACAGTGGATGGGCTGGATAAACCCCAACACTGGAGAGGCCAACATTT	QVQLQQSGPBLKKPGETVKVTCKTSGYTFT 30	PstI CAGGTCCAACTGCAGCAGCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGGTCACCTGCAAGACTTCTGGATATACCTTCACA CAGGTCCAACTGCAGCTGCAGCCTGAGCTGAAGAAGCCTGGAAGACCTCTCTGGAAGACAGTCCAGTTCCAGTGGAAGACTTCTAAAGACCTATATGGAAGTGT GTCCAGGTTGACGTCGTCAGACCTGGACTTCTTCGGACCTTCTCTGTCAGTTCCAGTTCCAGTGGAAGACCTTATATGGAAGTGT
7	00	99	70	59	80	30	90

001.1505876.1

Figure 2B

rigure	2B			× .				
Y F C S Q S S H V P P T F G A G T K L E J K R CDR3	BglII/BclI TATTTCTGCTCTAAAGTTCACATGTTCCTCCCACGTTCGGTGCTGGGACCAAGCTGGAGATCAAAACGT	SGVPDRESGSGSGTDFTLKISRVEARDLGL	TCTGGGGTCCCAJACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGTAGAGTGGAGGCTGAGGATCTGGGACTT+ AGACCCCAGGGTTTGTCCAAGTCACCGTCACCTAGTCCCTGTCTAAAGTGTGAGTTCTAGTCATCTCACCTCCGACTCCTAGACCCTGAA	HRHGMTYLHWYLQKPGQSPKLLIYTVSNRF	CACAGAAATGGAAACACCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGGCCAGTCTCCAAAGCTCCTGATCTACACAGTTTCCAACCGATTT	DIQLTQTPLSLPVSLGDQASESC <mark>RSSQSLV</mark>	FYUII GACATULTIGUAGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTTGCAGATCTAGTCAGAGCCTTGTA CTGTAGGACCTTGGGGTTTGAGGTGAGAGGGACGGACAGTCAGAACCTCTAGTTCGGAGGTAGAGACGTCTAGATCAGTCTCGGAACAT	
108	339	85	270	ស	180	27C	90	

Atty. Dkt. No.: 018733-1302

Figure 3A

н н н	WGQGSLVTVSS	NEWM
н н н	••••T••TVSS	CLL1VH
ш ш ш	••••••TVSS	hLL1VH
102 102 102	LQISSLKADDTAVYYCAREDSNGYKIFDY  ••••N••NE•MGT•F•S•SRGKNEAW•A•	RF-TS3 cLL1VH hLL1VH
79 79	PGQGLEWMGWINTNTGNPTYAQGFTGRFVFSLDTSVSTAY ••E••Q•••••••E••FDDD••••A•••ES•A•••F	RF-TS3 CLL1VH hLL1VH
4 4	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMNWVRQA	RF-TS3
0 4	QVQLQ•••P••••ET•••T••T••••N•GV••IK•T	cLL1VH
0 0	QVQLQ•••••••••••N•GV••IK••	hLl1VH

Atty. Dkt. No.: 018733-1302

gure 3B 다 다 뛰	HF.	hr cr hr
HF-21/28 CLL1Vk hLL1Vk	HF-21/28 CLL1Vk hLL1Vk	HF-21/28 CLL1Vk hLL1Vk
SRVEAEDVGVYYCMQGTHWPFTFGQGTRLEI ••••••L••F•S•SS•V•P•••A••K••IKR ••••••IKR	FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKI YL•••••KL••T•••F••••••••••••••••••	DVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW DIQLTS.DQRNH. DIQLS.DQ
106 108 108	75 75 75	ω ω ω ຫ ຫ ຫ

Figure 4A

	CDR3		
113	Y F C S R S R G R N R A W F A Y M G Q G T L V T V S S	7 A V	
360	ACTGCCGTGTATTTCTGTTCAAGATCGAAGGGTAAAAACGAAGCCTGGTTTGCTTATTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA	ACTGCCGTGT TGACGGCACA	
. 89	PKGRFAFSLDTSVSTAYLQISSLKADD	ם פ	
270	GATGATGACTTCAAGGGACGATTTGCCTTCTCCTTGGACACCTCTGTCAGCACGGCATATCTCCAGATCAGCAGCCTAAAGGCTGACGAC 270 CTACTACTGAAGTTCCCTGCTAAACGGAAGAGGAACCTGTGGAGACAGTCGTGCCGTATAGAGGTCTAGTCGTCGGATTTCCGACTGCTG	GATGATGACT	
59	VNWIKQAPGQGLQWMGWINPHTGBPTFCDR2	N Y G	
180	AACTATGGAGTGAACTGGATAAAGCAGGCCCCTGGACAAGGGCTTCAGTGGATGGGCTGGATAAACCCCAACACTGGAGAGACAACATTT	AACTATGGAG	
30	LQQSGSBLKKPGASVKVSCKASGYTFT	Q V Q	
90	CAGGTCCAACTGCAGCAATCTGGGTCTGAGTTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCTTCTGGATACACCTTCACT  90 GTCCAGGTTGAC3TCGTTAGACCCCAGACTCCAACTTCTTCGGACCCCGGAGTCACTTCCAAAGGACGTTCCGAAGACCTATGTGGAAGTGA	CAGGICCAAC	
		hLL1VH	

Figure 4B

Y F C S Q S S N V P P T F G A G T R L E I K R	TATTTCTGCTCTTAAAGTTCACATGTTCCTCCCACGTTCGGTGCTGGGACACGACTGGAGATCAAACGT	SGVPDRFSGSGTDFTLKISRVEABDVGV	TCTGGGGTCCCA3ACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAAATCAGCAGGGTGGAGGCTGAGGATGTTGGGGTT++ AGACCCCAGGGTCTGTCTAAGTCGCCGTCACCCAGTCCGTGACTAAAGTGTGACTTTTAGTCGTCCCACCTCCGACTCCTACAACCCCAA	HRNGNTYLHWF-QQRPGQSPRLLIYTVSNRF CDR1 CDR1	CACAGAAATGGAAACACCTATTTACATTGGTTTCAGCAGAGGCCAGGCCAATCTCCAAGGCCCCTGATCTACACAGTTTCCAACCGATTT+++++++	DIQLTQSPLSLPVTLGQPASISCRSSQSLV	GACATCCAGCTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCCATCTCCTGCAGATCAAGTCAAGTCAAGCCTTGTA+ CTGTAGGTCGACTGAGTCAGAGGTGAGAGGGACGGGCAGTGGGAACCTGTCGGCCGGAGGTAGAGGACGTCTAGTTCAGTCTCGGAACAT	
108	339	8.5	270	55	180	28C	90	

hLL1Vk

Figure 5

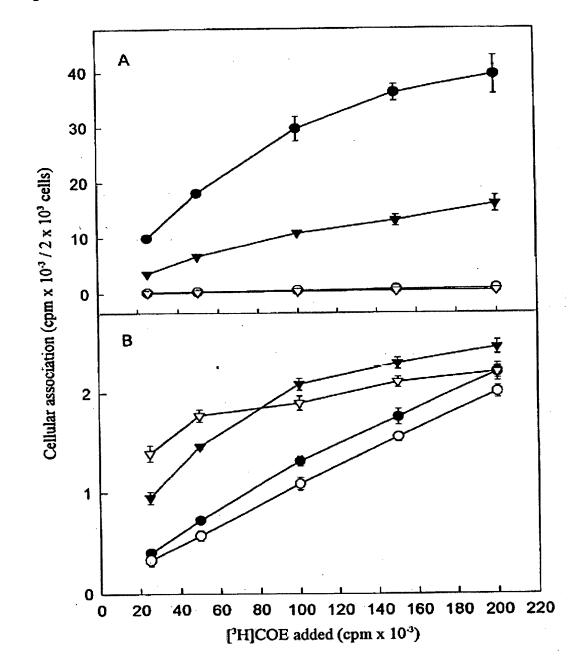


Figure 6

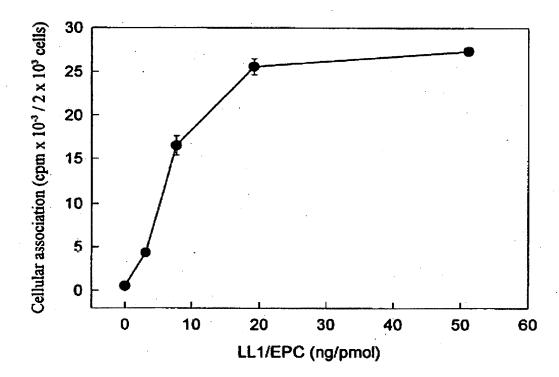


Figure 7

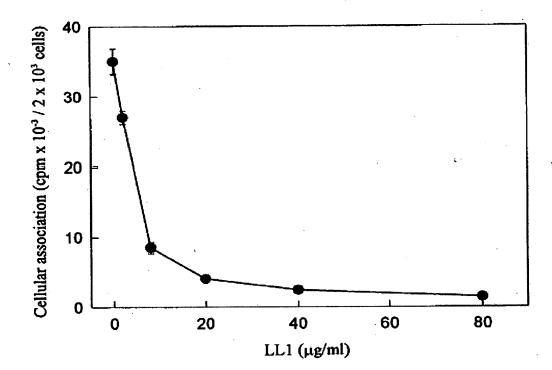


Figure 8

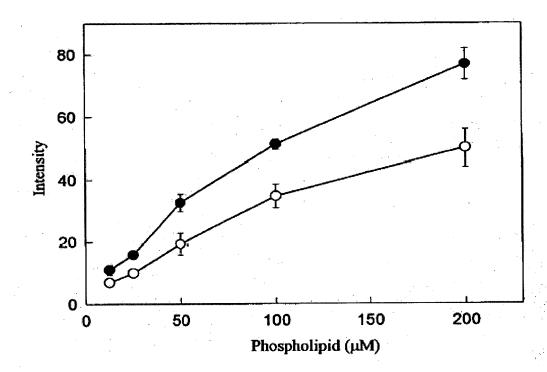


Figure 9

